WHAT IS CLAIMED IS:

1. A screening and/or quantification method of one or more activated transcriptional factor(s) (1) present in a cell or cell lysate, said method comprising the steps of:

binding to an insoluble solid support (3) double- stranded DNA sequence(s) (2) at the concentration of at least 0.01 pmole/cm2 of said solid support surface, said double-stranded DNA sequence(s) comprising a specific sequence able to bind said transcriptional factor and being linked to a spacer having a length of at least 6.8 nm,

putting into contact said transcriptional factor (1) with said bound double-stranded DNA sequence(s) (2); and

identifying and/or quantifying a signal resulting from the binding of said transcriptional factor(s) (1) upon said double-stranded DNA sequence(s) (2) and resulting from one characteristic specific of the transcriptional factor activation.

2. The method according to the claim 1, wherein said characteristic specific of the transcriptional factor (1) activation is a phosphorylation or dephosphorylation of amino acids of the transcriptional factor (1).

3. The screening and/ or quantification method according to the claim 1, wherein the characteristic specific of the transcriptional factor (1) activation is a binding of the transcriptional factor (1) to a protein which is part of its active complex.

4. The method according to the claim 3, wherein the protein is an activator or an inhibitor of the transcriptional factor (1) activation.

5. The method according to the claim 1, wherein the signal resulting from the binding of the transcriptional factor (1) upon the double-stranded DNA sequence(s) (2) and from at least one characteristic specific of the transcriptional factor (1) activation is detected by using

firstly a primary antibody (4) or an hypervariable portion thereof specific for the activated form of the transcriptional factor, and by

a secondary labelled antibody (5) directed against the primary antibody (4) or the specific hypervariable portion thereof.

6. The method of claim 5, wherein the secondary labelled antibody (5) is conjugated with an enzyme such as a peroxidase.

7. The method according to the claim 1, wherein the spacer corresponds to a double-stranded DNA sequence of at least 20 base pairs.

8. The method according to the claim 1, wherein the spacer corresponds to a chemical spacer of at least 10 atoms.

9. The method according to the claim 1, wherein the binding of the double-stranded DNA sequence(s) (2) to the insoluble solid support (3) is a covalent binding.

10. The method according to the claim 1, wherein the binding of the double-stranded DNA sequence(s) (2) to the insoluble solid support (3) is of non-covalent type and corresponds to a binding pair comprising a first element (6) and a second member (7), said first element being bound to the double-stranded DNA sequence, said second member (7) being bound to the surface of the solid support (3), said first element (6) being able to interact with said second member (7).

11. The method according to claim 10, wherein the binding pair is selected from the group consisting of biotin/streptavidin, hapten/receptor and antigen/antibody.

12. The method according to the claim 1, wherein the transcriptional factor is present in solution at a concentration lower than 20 nmolar (nM).

13. The method according to the claim 1, wherein the signal resulting from the binding of the transcriptional factor (1) upon the double-stranded DNA sequence(s) (2) and resulting from one characteristic specific of the transcriptional factor activation is a non radioactive resulting signal.

14. The method according to the claim 1, wherein the signal resulting from the binding of the transcriptional factor (1) upon the double-stranded DNA sequence(s) (2) and resulting from one characteristic specific of the transcriptional factor activation is obtained through an enzymatic reaction.

15. The method according to the claim 1, wherein multiple different transcriptional factors (1) are present in a same biological sample.

16. The method according to the claim 1, wherein the transcriptional factor (1) is selected from the group consisting of NF-KB, AP-1, CREB, SP-1, C/EBP, GR, HIF-1, Myc, NF-AT, Oct, TBP and CBF-1 or factors listed in table 1.

17. The method according to the claim 1, for the screening and/or quantification of multiple different transcriptional factors (1) upon a same support (3).

18. The method according to the claim 1, wherein the solid support (3) is an array bearing upon at least 4 spots/$cm^2$ of solid support surface, each spot containing double-stranded DNA sequence(s) (2) for the binding of transcriptional factor(s) (1).

19. The method according to the claim 1, wherein the double-stranded DNA sequence(s) fixed on the support surface contain in part or totally one or several of the consensus DNA sequences presented in the table 1.

20. The method according to the claim 1, wherein said transcriptional factor is the HIV integrase.

21. The method according to the claim 1, which further comprises the steps of screening, quantifying and/or recovering compounds able to bind to said transcriptional factor(s) or inhibit the binding of transcriptional factor(s) (1) to the specific sequence upon the double-stranded DNA sequence(s) (2) bound to said solid support (3).

22. The method according to the preceding claim 1, which further comprises the step of screening and/or quantifying a compound able to modulate the activity of said transcriptional factor by a modification of the level of the characteristic specific of the transcriptional factor activation.

23. The method according to the claim 1, which further comprises the steps of screening, quantifying and/or recovering compounds which modulate the binding and/or the activity of the said transcriptional factor(s) when they are put in contact with elements selected from the group consisting of cells, tissues or organisms.

24. The method according to the claim 1, which further comprises the steps of screening, quantifying and/or recovering compounds which modulate the activity of enzyme(s) or protein(s) acting on transcriptional factor(s) and then assayed for the activity of said transcriptional factor(s).

25. The method according to the claim 1, which further comprises the step of identification of transcriptional factor(s) and/or of peptides which are part of their active complex.

26. The method according to the claim 1, which further comprises the step of adding in the cell lysate an externally added transcriptional factor or a compound which is able to bind to a consensus sequence.

27. A kit for the screening and/ or quantification of transcriptional factor(s) (1) or (a) compound(s) able to bind to said transcriptional factor(s) (1) or inhibit the binding of said transcriptional factor(s) to a specific nucleotide sequence, which comprises double-stranded DNA sequence(s) (2) bound to an insoluble solid support (3) via a spacer having a length of at least 6.8 nm, at a concentration of at least 0.01 pmole/$cm^2$ of solid support surface (3) and a primary antibody or a specific hypervariable portion thereof, both being specific for the activated form of the transcriptional factor(s) (1) and possibly a second labelled antibody (5) directed against the primary antibody (4) or the specific hypervariable portion thereof.

28. The kit according to the claim 27, wherein said secondary labelled antibody (5) is conjugated with an enzyme such as a peroxidase.

29. The kit according to the claim 27, comprising a solid support bearing on its surface one or several double-stranded DNA consensus sequences at a concentration of at least 0.01 pmole/$cm^2$ comprising in part or totally one or several of the consensus sequence(s) listed in table 1 allowing the binding of a transcriptional factor present in solution and its detection and/or quantification.

30. The kit according to the claim 27, wherein the solid support is an array having at least 4 spot/$cm^2$ of solid support surface containing double-stranded DNA sequence(s) (2) for the binding of the transcriptional factor(s) (1).

31. The kit according to the claim 27, wherein said spacer is a double-stranded DNA nucleotide sequence of at least 20 base pairs.

32. The kit according to the claim 27, wherein said spacer is a double-stranded DNA nucleotide sequence of at least 40 base pairs.

33. The kit according to the claim 27, wherein the double-stranded DNA sequence (2) is bound to a first member (6) of a binding pair, able to interact with a second member (7) of the binding pair bound to the surface of the solid support (3).

34. The kit according to the claim 27, wherein the double-stranded DNA sequence (2) is covalently bound to the surface of the solid support.

35. The kit according to the claim 27, being a high-throughput screening device.